MAR 0 5 2001
PATENT & TRADEMARK OFFICE

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Paula M. Vertino
Serial No:	09/691,763
Filed:	October 18, 2000
For:	TMS1 COMPOSITIONS AND METHODS OF USE
Examiner:	Not Assigned
Group No.:	1645

CERTIFICATE OF MAILING UNDER 37 C.F.R. §1.8(a)

The undersigned hereby certifies that this document is being placed in the United States mail with first-class postage attached, addressed to Box Sequence, the Commissioner of Patents and Trademarks, Washington, D.C. 20231, on the 28 day of February, 2001.

Maryanne Trevisan

BOX Sequence
Commissioner of Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. §1.821(f)

Sir:

This statement is made pursuant to 37 CFR 1.821(f). Applicant encloses herewith an corrected written copy of the Sequence Listing and a corrected computer readable diskette. Applicant's attorney states that the information recorded in the computer readable form is identical to the written Sequence Listing and that the Sequence Listing contains no new matter.

Respectfully submitted,

Edward R. Gates
Reg. No. 31,616
Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
Boston, Massachusetts 02210
Tel.: 617-720-3500

DATE: 2/28/01
Attorney's Docket No.: E0355/7003 (ERG/MAT)

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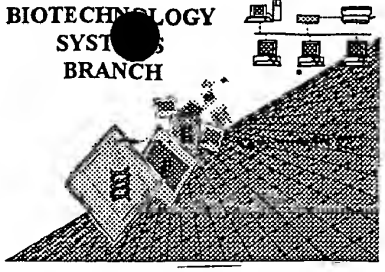
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/691,763

Source: OIPE

Date Processed by STIC: 10/29/2000

RECEIVED
MAR 13 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING DATE: 10/27/2000
PATENT APPLICATION: US/09/691,763 TIME: 10:01:33

Input Set : A:\E03557003.txt
Output Set: N:\CRF3\10272000\I691763.raw

Does Not Comply
Corrected Diskette Needed

```
   4 <110> APPLICANT: Vertino, Paula M.
   6 <120> TITLE OF INVENTION: TMS1 Compositions and Methods of Use
   9 <130> FILE REFERENCE: E0355/7003/ERG/MAT
OK> 11 <140> CURRENT APPLICATION NUMBER: US/09/691,763
OK> 11 <141> CURRENT FILING DATE: 2000-10-18
  11 <150> PRIOR APPLICATION NUMBER: US 60/159,975
  12 <151> PRIOR FILING DATE: 1999-10-18
  14 <160> NUMBER OF SEQ ID NOS: 27
  16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

ERRORED SEQUENCES

```
 190 <210> SEQ ID NO: 5                                          340
 191 <211> LENGTH: 339
 192 <212> TYPE: DNA
 193 <213> ORGANISM: Homo Sapiens
 195 <220> FEATURE:
 196 <221> NAME/KEY: CDS
 197 <222> LOCATION: (67)...(339)
 199 <400> SEQUENCE: 5
 200  ccgacttcct cctggtcggc ggctgcagcg gggtgagcgg cggcagcggc cggggatcct     60
 201  ggaggc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg gag aac       108
 202        Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
 203          1               5                  10
 205  ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg      156
 206  Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
 207   15                  20                  25                  30
 209  ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc      204
 210  Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
 211                  35                  40                  45
 213  atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag      252
 214  Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
 215              50                  55                  60
 217  acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg      300
 218  Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
 219          65                  70                  75
 221  cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g              340
 222  Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
E--> 223      80                  85                  90
 245 <210> SEQ ID NO: 7                                          057(next page)
 246 <211> LENGTH: 58
 247 <212> TYPE: DNA
 248 <213> ORGANISM: Homo Sapiens
 250 <220> FEATURE:
 251 <221> NAME/KEY: CDS
 252 <222> LOCATION: (3)...(58)
                                                                  (56)
```

```
     254 <400> SEQUENCE: 7
     255  gc tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca        47
     256     Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
     257     1               5                   10                  15
     259  gcc aag cca g                                                      57
E--> 260  Ala Lys Pro
     685 <210> SEQ ID NO: 26
     686 <211> LENGTH: 414 405
     687 <212> TYPE: DNA
     688 <213> ORGANISM: Homo Sapiens
     690 <220> FEATURE:
     691 <221> NAME/KEY: CDS
     692 <222> LOCATION: (75)...(404)
     694 <400> SEQUENCE: 26
     695  ccacgcgtcc gacttcctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg     60
     696  gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg      110
     697            Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
     698            1               5                   10
     700  gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg      158
     701  Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
     702          15                  20                  25
     704  tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg      206
     705  Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
     706       30                  35                  40
     708  ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac      254
     709  Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
     710   45                  50                  55                  60
     712  ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg      302
     713  Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
     714                  65                  70                  75
     716  ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc      350
     717  Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
     718              80                  85                  90
     720  tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc      398
     721  Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
     722          95                  100                 105
     724  aag cca g                                                          405
     725  Lys Pro
E--> 726  110
```

See next page for more errors

<210> 23
<211> 171
<212> PRT
<213> Rattus Norvegicus

<400> 23

```
Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
 1               5                  10                  15
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
            20                  25                  30
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
        35                  40                  45
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
    50                  55                  60
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65                  70                  75                  80
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
                85                  90                  95
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
            100                 105                 110
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
        115                 120                 125
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
    130                 135                 140
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145                 150                 155                 160
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser
                165                 170
```

see item 10 on Error Summary Sheet

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 10/27/2000
PATENT APPLICATION: US/09/691,763 TIME: 10:01:35

Input Set : A:\E03557003.txt
Output Set: N:\CRF3\10272000\I691763.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:223 M:252 E: No. of Seq. differs, <211>LENGTH:Input:339 Found:340 SEQ:5
L:260 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:260 M:252 E: No. of Seq. differs, <211>LENGTH:Input:58 Found:57 SEQ:7
L:306 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:527 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:527 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:559 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 22
L:575 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23
L:575 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:575 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:575 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:575 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:726 M:252 E: No. of Seq. differs, <211>LENGTH:Input:414 Found:405 SEQ:26